Technical appendix

Bootstrapping of outbreak data to estimate the proportion of cases due to foodborne transmission

For each pathogen, we estimated the proportion of cases attributable to foodborne transmission by bootstrapping 4,999 replicate samples from the outbreak dataset and obtaining an empirical distribution for the proportion of cases involved in foodborne outbreaks. For *Giardia* and *Cryptosporidium*, this gave unrealistically high values for the proportion attributable to foodborne transmission and we instead based our estimates on the proportion of outbreaks that were foodborne. We summarised the resulting distributions by fitting a Beta distribution using maximum likelihood.

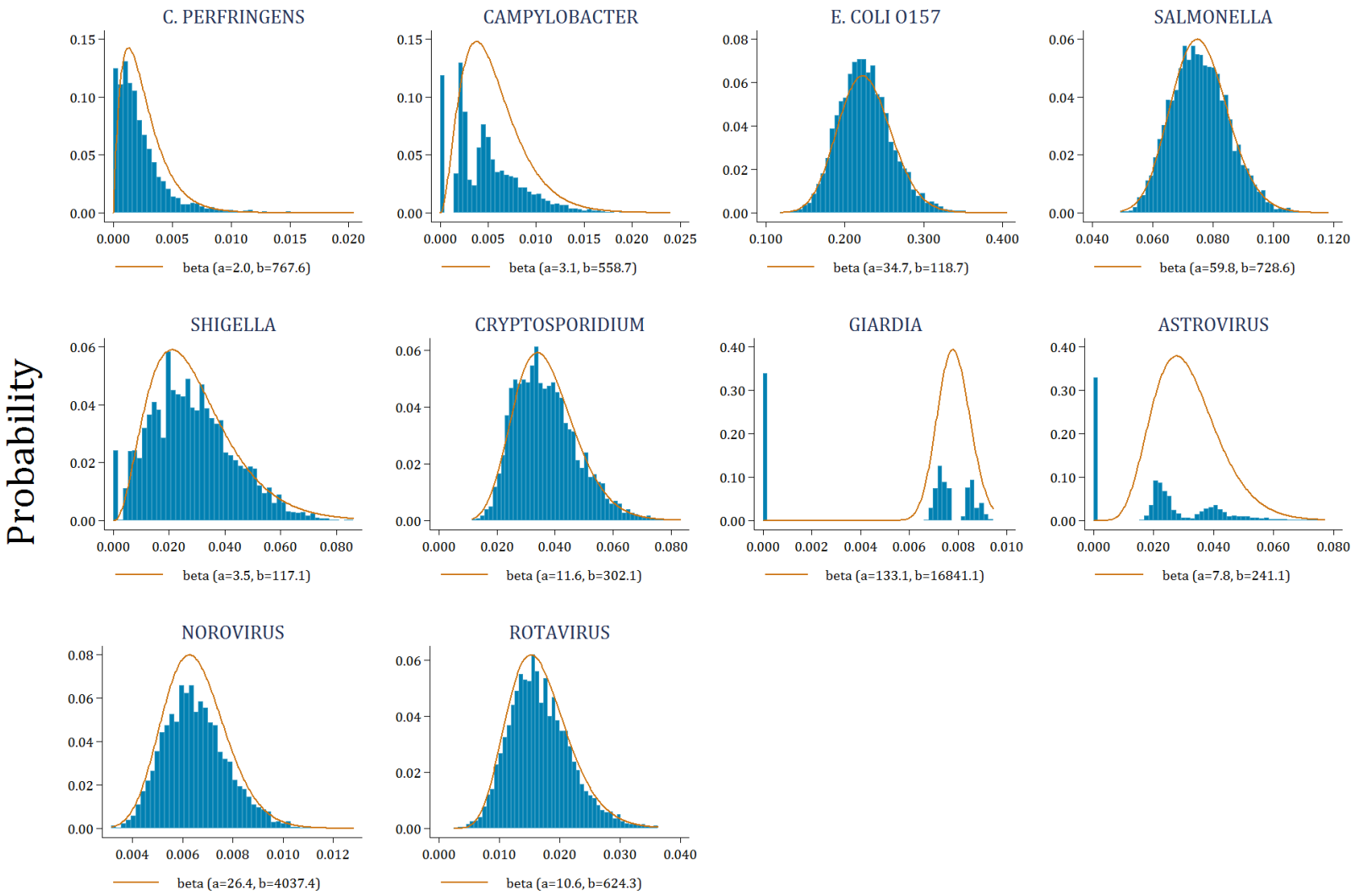
For *Listeria*, for which the six cases observed were all from outbreaks involving foodborne transmission, we set a lower boundary for the proportion foodborne by assuming that the next outbreak observed, involving two cases, would not be foodborne. This is based on the definition for a general outbreak as an incident involving two or more epidemiologically-related cases. We then drew values at random from a Binomial distribution with 8 observations and 6 successes and fitted a Beta function to the resulting distribution. Similarly, for astrovirus, for which no foodborne outbreaks were reported, we set an upper boundary for the proportion foodborne by assuming that the next outbreak, involving two cases, would be foodborne, and derived Beta parameters in a similar fashion. The parameters from the fitted Beta distributions were then used in the Monte Carlo simulation. For adenovirus and sapovirus, for which no outbreaks were reported, we used Beta parameters derived from analysis of rotavirus and norovirus outbreaks respectively.

Bootstrapping of outbreak data to estimate the proportion of cases hospitalised

Data on hospitalisation in outbreaks were only available from England and Wales. For each reported outbreak in the England and Wales dataset (excluding outbreaks that occurred in hospitals and residential institutions), we calculated the proportion of outbreak cases that was hospitalised and plotted the resulting distribution for the proportion of cases hospitalised. We calculated this by causative organism and separately for all outbreaks and for foodborne outbreaks only. There was no major difference in hospitalisation between all outbreaks and foodborne outbreaks, so we based estimates of hospitalisation on data from all outbreaks. To account for uncertainty in hospitalisation parameters, we used a two-step approach. For each pathogen, we first obtained an empirical distribution for the proportion of cases hospitalised by bootstrapping 4,999 replicate samples of the outbreak data. For example, if there were 50 reported outbreaks for a given pathogen, we sampled 50 outbreaks with replacement from this set and calculated the mean proportion of cases hospitalised across the outbreak sample, weighted by outbreak size. This was repeated 4,999 times for each pathogen. The hospitalisation proportion was weighted by outbreak size because many reported outbreaks involve few cases and are therefore unlikely to involve hospitalised cases. The small number of larger outbreaks, on the other hand, is potentially more informative for estimating hospitalisation. We then fitted a Beta distribution to the bootstrapped data and estimated the corresponding a and b parameters using maximum likelihood. The mean hospitalisation proportions for each pathogen and Beta parameters used in Model 1 are given in Table A1. The fits of the Beta distributions to the outbreak data are show graphically in Figure A1.

For *Listeria*, all reported outbreaks occurred in hospitals, so it was not possible to estimate the hospitalisation rate from outbreaks. For adenovirus and sapovirus, no outbreaks were reported. For these two pathogens, parameters based on analysis of rotavirus and norovirus outbreaks respectively were used. Bootstrap estimates with fitted Beta distributions for the remaining 10 pathogens are shown below.

Figure A1: Bootstrap estimates of the proportion of cases hospitalised with fitted Beta distributions (shown by red line) by pathogen, UK outbreak data 2001-08



Deriving priors for the proportion hospitalised (γ_p) from the IID1 and IID2 Studies

We pooled data from the IID1 and IID2 Studies and calculated, by pathogen, the proportion of cases presenting to the GP that were hospitalised. Applying this proportion to the rate of GP consultation gave an estimate of the hospitalisation rate. For each pathogen, we used the ratio of this rate to the rate of community IID to obtain an estimate of the proportion of cases hospitalised. This approach implicitly assumes that hospitalised cases always consult a GP. This is reasonable in the UK, as hospitalisation is likely to occur through a GP referral, but potentially disregards a fraction of more severe cases (e.g. cases admitted as a result of an emergency hospital visit). However, it was not possible to estimate hospitalisation directly from the IID1 and IID2 community cohort study components, as hospitalisation is very uncommon and the two cohort studies were not designed to measure the rate of hospitalisation.

To account for uncertainty in the hospitalised proportion, we took 100,000 random samples from the distributions of the overall IID rate, c_p, and the proportion of GP cases hospitalised, and fitted a Beta function to the resulting distribution for the hospitalised proportion using maximum likelihood methods. The estimated parameters from this Beta distribution were used to inform the prior values for γ_p in the Bayesian approach (Table A2). For VTEC O157, for which hospitalisation information was not available from IID1 and IID2, we used a non-informative prior defined by the distribution Beta(1,1). For pathogens for which no hospitalisations were observed in the IID1 and IID2 studies, we specified limits to the fitted Beta distributions by assuming that the next case observed would have been hospitalised. Thus, for *Shigella*, with 11 cases and no hospitalisations, we obtained Beta parameters for a distribution with a mean equivalent to 1/12=0.087. Empirical bootstrap distributions with fitted Beta functions are shown below.

Monte Carlo approach (Model 1)

We obtained estimates of F_p, G_p and H_p using Monte Carlo simulation, each time drawing at random from each parameter distribution in the model. We carried out 100,000 simulations, discarding the first 10% and retaining the model outputs for every 10th simulation. We checked model convergence graphically by plotting parameter values over time to verify adequate mixing, plotting autocorrelograms and comparing density plots for outcome variables by tertile of the simulation chain. The model and associated parameter distributions are described below:

$$F_p = N \cdot c_p \cdot \pi_p$$
$$G_p = N \cdot g_p \cdot \pi_p$$
$$H_p = F_p \cdot \gamma_p$$

$$\log(c_p) \sim N(\mu_{cp}, \sigma_{cp})$$

$$\log(g_p) \sim N(\mu_{gp}, \sigma_{gp})$$

$$\pi_p \sim \text{Beta}(a_{\pi p}, b_{\pi p})$$

$$\gamma_p \sim \text{Beta}(a_{\gamma p}, b_{\gamma p})$$

From the ensuing distributions of F_p, G_p and H_p, we used the median and central 95% of the distributions as the point estimates and 95% credible intervals respectively. Parameter values for each pathogen are given in table A1 below.

Bayesian approach (Models 2 and 3)

In the Bayesian approach, we included parameters for the prior distributions of π_p and γ_p. These priors were used, together with the outbreak data to obtain posterior distributions for these parameters, which were then used in the model as described below:

$$F_p = N \cdot c_p \cdot \pi_p$$
$$G_p = N \cdot g_p \cdot \pi_p$$
$$H_p = F_p \cdot \gamma_p$$

$$\log(c_p) \sim N(\mu_{cp}, \sigma_{cp})$$
$$\log(g_p) \sim N(\mu_{gp}, \sigma_{gp})$$
$$f_p \sim \text{Binomial}(\pi_p, o_p)$$
$$\pi_p \sim \text{uniform}(u_{\pi p}, v_{\pi p})$$
$$h_p \sim \text{Binomial}(\gamma_p, m_p)$$
$$\gamma_p \sim \text{Beta}(a_{\gamma p}, b_{\gamma p})$$

For each pathogen, p, the parameters f_p and o_p represent the number of cases involved in foodborne and all outbreaks respectively. Similarly, h_p and m_p represent the pathogen-specific number of hospitalisations and GP consultations as observed in IID1 and IID2. The prior values for parameters π_p and γ_p are defined by uniform and Beta distributions respectively as described above. In Model 2, the uniform distributions for π_p were informed by data from published multi-pathogen food attribution studies. We used a further model, Model 3, with the same structure as Model 2, but with parameters for the prior distribution of π_p being derived from case-control and food attribution studies from the literature review. A full description of parameters for models 2 and 3 is given in the technical appendix.

For each model, we carried out 100,000 simulations to obtain posterior distributions for F_p, G_p and H_p, discarding the first 10% and retaining the model outputs for every 10^{th} simulation. We checked for model convergence as described for the Monte Carlo approach above. Parameter values for each pathogen are given in tables A2 and A3 below.

Table A1: Parameter values for Model 1

	Incidence					Proportion foodborne				Proportion hospitalised			
Organism	μ_{cp}	σ_{cp}	μ_{gp}	σ_{gp}	**Source**	PF	$a_{\pi p}$	$b_{\pi p}$	**Source**	PH	$a_{\gamma p}$	$b_{\gamma p}$	**Source**
Bacteria													
C. perfringens	-6.50	0.49	-8.34	0.39	A	0.862	25.0	4.3	D	0.0017	2.0	767.6	D
Campylobacter	-4.68	0.22	-6.66	0.18	A	0.501	6.8	6.5	D	0.0046	3.1	558.7	D
E. coli O157	-8.11	1.36	-11.51	1.12	A	0.531	14.1	12.8	D	0.2235	34.7	118.7	D
Listeria	--	--	--	--	C	1.000	7.8	3.1	D	--	--	--	H
Salmonella	-7.42	0.71	-8.62	0.46	A	0.904	116.0	12.6	D	0.0751	59.8	728.6	D
Shigella	-9.29	0.97	-9.98	0.27	B	0.222	1.7	4.7	D	0.0260	3.5	117.1	D
Protozoa													
Cryptosporidium	-7.26	0.69	-8.52	0.45	A	0.051	4.0	73.2	D	0.0362	11.6	302.1	D
Giardia	-7.13	0.67	-9.32	0.56	A	0.167	4.0	11.8	D	0.0073	133.1	16,841.1	D
Viruses													
Adenovirus	-4.59	0.21	-7.08	0.28	A	--	4.8	230.3	F	--	10.6	624.3	F
Astrovirus	-5.24	0.29	-7.82	0.37	A	0.000	3.6	437.6	D	0.2222	7.8	241.1	D
Norovirus	-3.06	0.09	-6.18	0.19	A	0.025	38.7	1,473.6	D	0.0064	26.4	4,037.4	D
Rotavirus	-4.37	0.19	-6.60	0.21	A	0.014	4.8	230.3	D	0.0165	10.6	624.3	D
Sapovirus	-3.65	0.13	-6.46	0.19	A	--	38.7	1,473.6	G	--	26.4	4,037.4	G

PF: Proportion foodborne as estimated from outbreak data; PH: Proportion hospitalised as estimated from outbreak data

A: IID2 Study; B: 2009 laboratory reports * IID1 reporting ratio; C: 2009 laboratory reports

D: Outbreak data; F: No outbreak data available, assumed same as rotavirus; G: No outbreak data available, assumed same as norovirus

H: All reported Listeria outbreaks were in hospitals/residential institutions so hospitalisation parameters could not be estimated

Table A2: Parameter values for Model 2

	Proportion foodborne						Proportion hospitalised					
	Binomial likelihood			Uniform prior			Binomial likelihood			Beta prior		
Organism	f_p	o_p	**Source**	$u_{\pi p}$	$v_{\pi p}$	**Source**	h_p	m_p	**Source**	$a_{\gamma p}$	$b_{\gamma p}$	**Source**
Bacteria												
C. perfringens	1,691	1,964	D	0.761	1.000	[1–7]	2	1,120	D	1.6	277.1	J
Campylobacter	373	761	D	0.420	0.800	[1–7]	2	424	D	3.5	2,119.3	J
E. coli O157	564	1,041	D	0.400	0.760	[1–7]	197	877	D	1.0	1.0	K
Listeria	6	8	D	0.690	1.000	[1,4–6,8]	--	--	H	--	--	
Salmonella	7,128	7,892	D	0.550	0.950	[1–7]	419	5,527	D	1.2	75.3	J
Shigella	65	310	D	0.082	0.310	[1,5,6,9]	4	153	D	0.9	7.1	J
Protozoa												
Cryptosporidium	4	65	D	0.000	0.120	[1–3,5,9]	31	836	D	1.2	99.1	J
Giardia	1	7	D	0.050	0.300	[1–3,5,7]	1	137	D	1.2	150.4	J
Viruses												
Adenovirus	30	2,338	F	0.000	0.100	[1,2]	20	1,211	F	3.1	1,819.8	J
Astrovirus	2	285	D	0.005	0.107	[1,2,5]	2	88	D	2.5	1,252.6	J
Norovirus	1500	58,855	D	0.000	0.390	[1–3,5–7,9,10]	80	12,333	D	3.2	6,124.2	J
Rotavirus	30	2,338	D	0.005	0.130	[1–3,5,7]	20	1,211	D	3.6	1,295.6	J
Sapovirus[1]	1500	58,855	G	--	--		80	12,333	G	3.9	3,072.6	J

Incidence parameters are the same as those for Model 1

[1] Estimates for sapovirus could not be calculated from this model because of the lack of published data to inform prior parameters

D: Outbreak data; F: No outbreak data available, assumed same as rotavirus; G: No outbreak data available, assumed same as norovirus

H: All reported Listeria outbreaks were in hospitals/residential institutions so hospitalisation parameters could not be estimated

J: IID1 and IID2 GP Presentation Studies; K: Non-informative Beta distribution used

Table A3: Parameter values for Model 3

	Proportion foodborne						Proportion hospitalised					
	Binomial likelihood			Uniform prior			Binomial likelihood			Beta prior		
Organism	f_p	o_p	**Source**	$u_{\pi p}$	$v_{\pi p}$	**Source**	h_p	m_p	**Source**	$a_{\gamma p}$	$b_{\gamma p}$	**Source**
Campylobacter	373	761	D	0.110	1.000	[11–26]	2	424	D	3.5	2,119.3	J
E. coli O157	564	1,041	D	0.090	0.642	[13,27–29]	197	877	D	1.0	1.0	K
Listeria	6	8	D	0.180	1.000	[30,31]	--	--	H	1.0	1.0	K
Salmonella	7,128	7,892	D	0.090	1.000	[13,32–34]	419	5,527	D	1.2	75.3	J

Incidence parameters are the same as those for Model 1

D: Outbreak data

H: All reported Listeria outbreaks were in hospitals/residential institutions so hospitalisation parameters could not be estimated

J: IID1 and IID2 GP Presentation Studies; K: Non-informative Beta distribution used

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